

03 FILE COPY

MPEERH
(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 2 14:43:26 1998; MasPar time 11.79 Seconds
560.820 Million cell updates/sec

Tabular output not generated.

Title: US08-851-843-83
Description: (1-157) from-US08851843.pep
Perfect Score: 1179
Sequence: 1 FFYCTEISSVTIVYERHDT.....FNNVLPYEMKFDVKSCYD 157

Scoring table: PAM 150
Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1 sp_fungi 2 sp_human 3 sp_invertebrate 4 sp_mammal
5 sp_mhc 6 sp_organelle 7 sp_phase 8 sp_plant
9 sp_bacteria 10 sp_rodent 11 sp_virus 12 sp_vertibrate
13 sp_unclassified

Statistics: Mean 43.179; Variance 84.407; scale 0.512

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Re	Score	Match	Length	ID	Description
1	1179	100.0	884	1 Q06163	CHROMOSOME XII COSMID
2	159	13.5	988	1 Q13339	TELOMERASE REVERSE TRA
3	159	13.5	1031	3 Q00939	TELOMERASE SUBUNIT P12
4	157	13.3	989	1 Q13338	TELOMERASE REVERSE TRA
5	147	12.5	1132	2 Q14746	TELOMERASE REVERSE TRA
6	147	12.5	1132	2 Q14783	TELOMERASE CATALYTIC S
7	103	8.7	336	9 Q52228	PROTEIN D123
8	102	8.7	336	9 Q52228	REPLICATION-ASSOCIATED
9	103	8.7	504	9 Q34044	ORF13
10	102	8.7	1057	12 Q13033	RECOMBINASE
11	101	8.6	349	6 Q02593	HYPOTHETICAL 40.2 KD P
12	100	8.5	620	10 P97524	VERY-LONG-CHAIN ACYL-C
13	99	8.4	344	9 Q28645	TRANSPOSASE, PUTATIVE
14	99	8.4	620	10 Q35488	VERY-LONG-CHAIN ACYL-C
15	98	8.3	206	9 Q27039	ATP SYNTHASE, SUBUNIT
16	97	8.2	620	2 Q14975	VERY-LONG-CHAIN ACYL-C
17	95	8.1	132	11 P89129	AC3 PROTEIN
18	96	8.1	132	11 P89129	TRANSPOSASE, PUTATIVE
19	95	8.1	183	4 Q29014	ALPHA-1 ACID GLYCOPROT
20	96	8.1	362	11 Q88419	SPV1-C74, COMPLETE GEN

21	95	8.1	370	8 Q40093	PNIL34.	1.05e+00
22	96	8.1	530	3 Q17404	AC3.8.	7.78e-01
23	95	8.1	1280	9 Q45849	BOTULINUM NEUROTOXIN.	1.05e+00
24	94	8.0	455	1 Q08231	CHROMOSOME XV READING	1.41e+00
25	94	8.0	661	9 Q31849	YOJO PROTEIN.	1.41e+00
26	94	8.0	710	3 Q23334	ZC455.4.	1.41e+00
27	94	8.0	1547	3 Q16140	TOPOISOMERASE II (EC 5	1.41e+00
28	93	7.9	160	9 Q45198	ALTERNATIVELY SPLICED	1.89e+00
29	93	7.9	277	7 Q38606	ORF2 (FRAGMENT).	1.89e+00
30	93	7.9	517	11 Q98160	ORF2, UNKNOWN.	1.89e+00
31	93	7.9	875	9 Q31978	YOMG PROTEIN.	1.89e+00
32	93	7.9	2033	2 Q92817	ENVOLPAIN.	1.89e+00
33	92	7.8	305	9 Q32798	PUTATIVE MEMBRANE PROT	2.53e+00
34	92	7.8	305	9 Q32796	ORFA PROTEIN.	2.53e+00
35	92	7.8	516	4 Q29526	LIVER CYTOCHROME P450	2.53e+00
36	92	7.8	943	3 Q23670	K12D12.1 (FRAGMENT).	2.53e+00
37	92	7.8	1823	12 Q91062	VITELLOGENIN PRECURSOR	2.53e+00
38	91	7.7	360	3 Q25888	CATHEPSIN L-LIKE CYSTE	3.38e+00
39	91	7.7	365	3 Q23200	W06D11.4.	3.38e+00
40	91	7.7	467	8 Q04127	LETHAL LEAF-SPOT 1 (FR	3.38e+00
41	91	7.7	539	3 Q16514	TP5H4.9 PROTEIN.	3.38e+00
42	90	7.6	309	9 Q06036	EP5H.	4.50e+00
43	90	7.6	532	11 Q65876	ORF2 (FRAGMENT).	4.50e+00
44	90	7.6	602	9 Q25122	GTP-BINDING MEMBRANE P	4.50e+00
45	89	7.5	1612	10 Q64399	DNA TOPOISOMERASE (ATP	5.97e+00

ALIGNMENTS

RESULT 1
ID Q06163 PRELIMINARY; PRT: 884 AA.
AC Q06163;
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMREL. 01, LAST ANNOTATION UPDATE)
DE CHROMOSOME XII COSMID 8543.
GN L8543.12.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA DU Z.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,
RA KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
RA JOHNSON D., JOHNSON L., LANGSTON Y., LATREILLE P., LE T.,
RA MARDIS E., MENEZES S., MILLER N., NEAN M., PAULEY A., PELUSO D.,
RA RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D.,
RA WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA WATERSTON R.;
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U20618; G662136; -;
SQ SEQUENCE 884 AA; 102663 MW; 1A94320F CRC32;

Query Match 100.0%; Score 1179; DB 1; Length 884;
Best Local Similarity 100.0%; Pred. No. 1.10e-218;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 380 FFYCTEISSVTIVYERHDTWNKLIITPFIVEYKTVLVNNVCRNHNSTLSNFSKMR 439
QY 1 FFYCTEISSVTIVYERHDTWNKLIITPFIVEYKTVLVNNVCRNHNSTLSNFSKMR 60
Db 440 IIPKKNNFRIIAICPGADEEFTIYKRNHKNAIQTKILEYLRNKRPTSTFKIYSP 499

QY 61 IIPKSNNEFRIIAIPCGADEEEFTYKENHKNAIQPTQKILEYLRNKRPTFTKIYSP 120

Db 500 TQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYD 536
 |||||
 QY 121 TQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYD 157
 |||||

RESULT 2
 ID O13339 PRELIMINARY; PRT; 988 AA.
 AC O13339;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TELOMERASE REVERSE TRANSCRIPTASE 1.
 GN TRT1.
 OS SCHIZOSACHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
 RA LINGNER J., HARLEY C.B., CECH T.R.;
 RL SCIENCE 277:955-959(1997).
 DR EMBL; AF015783; G2340168;
 KW RNA-DIRECTED DNA POLYMERASE.
 SQ SEQUENCE 988 AA; 116328 MW; 39C385A7 CRC32;

Query Match 13.5%; Score 159; DB 1; Length 988;
 Best Local Similarity 27.8%; Pred. No. 2.57e-10;
 Matches 45; Conservative 36; Mismatches 68; Indels 13; Gaps 12;

Db 443 FFYITESDLNRVTYFRKDIWKLLCRPFTSMKAEKINENNVRM-DTQK-TTLPPA 500
 |||||
 QY 1 FFYCTEISSTVT-IVYFRHDTWNLITPFIVEY-FKTYL-VENNVCRNHSYTLNENHS 57
 |||||

Db 501 VIRLLPKK-NF-FRLTNLKRFLIKGSKNKKMLVSTNOTLRPVASILKHLNESSGIP 558
 |||||
 QY 58 KRIIPKSNNEFRIIA-IPCG-ADDEEFTYKENHKNAIQPTQKILEYLRNKRPTFT 115
 |||||

Db 559 --FN-LEVYMKLLTFKKDLKH-RMFGKKYFVRIDIKSCYD 596
 |||||
 QY 116 KIYSPQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYD 157
 |||||

RESULT 3
 ID O00939 PRELIMINARY; PRT; 1031 AA.
 AC O00939;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TELOMERASE SUBUNIT P123.
 OS EUCALYPTUS AEDICULATUS.
 OC EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; ALVEOLATA; CILIOPHORA;
 OC HYPOTRICHES; EUPLOTIDA; EUPLOTES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97274210.
 RA LINGNER J., HUGHES T.R., SHEVCHENKO A., MANN M., LUNDBLAD V.,
 RA CECH T.R.;
 RL SCIENCE 276:561-567(1997).
 DR EMBL; U95964; G2072336;
 SQ SEQUENCE 1031 AA; 122562 MW; 21A885CD CRC32;

Query Match 13.5%; Score 159; DB 3; Length 1031;
 Best Local Similarity 24.7%; Pred. No. 2.57e-10;
 Matches 40; Conservative 39; Mismatches 71; Indels 12; Gaps 10;

Db 455 FFYVTEQOKSYKTYIRKNIWDVIMKMSADLKKETLAEVQOE-KEVEEKKSLGTPAGK 513
 |||||
 QY 1 FFYCTEISSTVTIYF-RHDTWNLKLTIPFIVEYFKTYLVNNVCRNHSYTLN-ENHSH 58
 |||||

Db 514 LRLIPKKT--FRPIMTNKKIYNSDKTT-KLTNTKLNLSHMLKTLKRNMFKDPFG- 569
 |||||

QY 59 MRIIPKSNNEFR-IIAIPCGADEEEFTYKENHKNAIQPTQKILEYLRNKR-PTSFTK 116

Db 570 -FAVENYDDVMKKYEE-FVCWKVQVQKPLFFATYMDIEKCYD 609
 |||||
 QY 117 IYSPQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYD 157
 |||||

RESULT 4
 ID O13338 PRELIMINARY; PRT; 989 AA.
 AC O13338;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TELOMERASE REVERSE TRANSCRIPTASE 1.
 GN TRT1.
 OS SCHIZOSACHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
 RA LINGNER J., HARLEY C.B., CECH T.R.;
 RL SCIENCE 277:955-959(1997).
 DR EMBL; AF015783; G2340169;
 KW RNA-DIRECTED DNA POLYMERASE.
 SQ SEQUENCE 989 AA; 116456 MW; FDE74202 CRC32;

Query Match 13.3%; Score 157; DB 1; Length 989;
 Best Local Similarity 28.8%; Pred. No. 5.50e-10;
 Matches 47; Conservative 36; Mismatches 66; Indels 14; Gaps 13;

Db 443 FFYITESDLNRVTYFRKDIWKLLCRPFTSMKAEKINENNVRM-DTQK-TTLPPA 500
 |||||
 QY 1 FFYCTEISSTVT-IVYFRHDTWNLITPFIVEY-FKTYL-VENNVCRNHSYTLNENHS 57
 |||||

Db 501 VIRLLPKK-NF-FRLTNLKRFLIKGSKNKKMLVSTNOTLRPVASILKHLNESSGI 558
 |||||
 QY 58 KRIIPKSNNEFRIIA-IPCGADEEEFTYKE-NHKN-AIOPTQKILEYLRNKRPTSF 114
 |||||

Db 559 P--FN-LEVYMKLLTFKKDLKH-RMFGKKYFVRIDIKSCYD 597
 |||||
 QY 115 TKIYSPQIADRIKEFKORLLKFNVLPELYFMKFDVKSCYD 157
 |||||

RESULT 5
 ID O14746 PRELIMINARY; PRT; 1132 AA.
 AC O14746;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TELOMERASE REVERSE TRANSCRIPTASE.
 GN HTRT.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
 RA LINGNER J., HARLEY C.B., CECH T.R.;
 RL SCIENCE 277:955-959(1997).
 DR EMBL; AF015950; G2330017;
 KW RNA-DIRECTED DNA POLYMERASE.
 SQ SEQUENCE 1132 AA; 126996 MW; 2DFBEDF3 CRC32;

Query Match 12.5%; Score 147; DB 2; Length 1132;
 Best Local Similarity 26.1%; Pred. No. 2.34e-08;
 Matches 43; Conservative 37; Mismatches 71; Indels 14; Gaps 14;

Db 560 FFYVTEQOKSYKTYIRKNIWDVIMKMSADLKKETLAEVQOE-KEVEEKKSLGTPAGK 618
 |||||
 QY 1 FFYCTEISSTVTIYF-RHDTWNLKLTIPFIVEYFKTY-LVE-NNV-CRNHNSYTLNENH 56
 |||||

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 2 14:14:03 1998; Maspar time 3.04 Seconds

Tabular output not generated. 72.151 Million cell updates/sec

Description: 38
Perfect Score: 38
Sequence: 1 DDFLXI 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.538; Variance 24.115; scale 0.852

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
2	38	100.0	115	2	A46242	T-cell receptor alpha	1.96e+02
3	38	100.0	185	2	H64031	hypothetical protein	1.96e+02
4	38	100.0	245	2	H89471	conserved hypothetical	1.96e+02
5	38	100.0	256	2	S37861	nitrogen fixation pro	1.96e+02
6	38	100.0	266	2	S74573	hypothetical protein	1.96e+02
7	38	100.0	269	2	S03715	T-cell receptor alpha	1.96e+02
8	38	100.0	337	2	S38166	hypothetical protein	1.96e+02
9	38	100.0	351	2	G70137	phospho-N-acetylmu	1.96e+02
10	38	100.0	364	2	S59885	H+-transporting ATP s	1.96e+02
11	38	100.0	365	2	S74847	hypothetical protein	1.96e+02
12	38	100.0	366	2	D69951	conserved hypothetical	1.96e+02
13	38	100.0	403	2	S41708	cyclin B3 - chicken	1.96e+02
14	38	100.0	412	2	JN0319	acid phosphatase (EC	1.96e+02
15	38	100.0	415	2	S04885	genome polyprotein -	1.96e+02
16	38	100.0	459	2	S76712	hypothetical protein	1.96e+02
17	38	100.0	464	2	C70122	thiophene and furan o	1.96e+02
18	38	100.0	462	2	A05026	hypothetical protein	1.96e+02
19	38	100.0	492	2	B64642	cell division protein	1.96e+02
20	38	100.0	499	2	S41599	cytochrome P450 77A1	1.96e+02
21	38	100.0	531	2	F84215	N-utilization substan	1.96e+02
22	38	100.0	884	2	S53396	hypothetical protein	1.96e+02
23	38	100.0	1118	2	S44641	F37A4.4 protein - Cae	1.96e+02
24	38	100.0	2230	1	GNNSYA	genome polyprotein -	1.96e+02

24	38	100.0	2368	2	S46005	ESR1 protein - yeast	1.96e+02
25	37	97.4	105	2	JL0083	T-cell receptor delta	3.03e+02
26	37	97.4	108	2	JH0336	T-cell receptor alpha	3.03e+02
27	37	97.4	187	2	S49755	adenine phosphoribosy	3.03e+02
28	37	97.4	255	2	S69805	hypothetical protein	3.03e+02
29	37	97.4	285	2	S60598	collagen alpha chain	3.03e+02
30	37	97.4	293	1	RGBY54	translation activator	3.03e+02
31	37	97.4	331	2	S72868	hypothetical protein	3.03e+02
32	37	97.4	337	2	C64434	hypothetical protein	3.03e+02
33	37	97.4	378	2	H69505	conserved hypothetical	3.03e+02
34	37	97.4	380	1	RGHUA1	GTP-binding regulator	3.03e+02
35	37	97.4	394	1	RGBOGA	GTP-binding regulator	3.03e+02
36	37	97.4	394	1	RGHYA2	GTP-binding regulator	3.03e+02
37	37	97.4	395	1	RGHUA2	GTP-binding regulator	3.03e+02
38	37	97.4	419	2	S34421	GTP-binding regulator	3.03e+02
39	37	97.4	473	2	S49939	probable membrane pro	3.03e+02
40	37	97.4	494	2	S24387	H+-transporting ATPas	3.03e+02
41	37	97.4	536	2	A36395	spore wall maturation	3.03e+02
42	37	97.4	676	2	F69394	H+-transporting ATP s	3.03e+02
43	37	97.4	937	2	A24878	DNA-directed DNA poly	3.03e+02
44	37	97.4	1175	2	F64489	hypothetical protein	3.03e+02
45	37	97.4	3092	2	S46009	GTPase-activating pro	3.03e+02

ALIGNMENTS

RESULT ENTRY TITLE	1	A46242	#type fragment
ORGANISM		T-cell receptor alpha chain variable region - mouse (fragment)	
DATE		21-Sep-1993	#sequence_revision 18-Nov-1994
ACCESSIONS		20-Mar-1998	#common_name house mouse
REFERENCE		Natarajan, K.; Burstyn, D.; Zauderer, M. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8874-8878	
#authors		Major histocompatibility complex determinants select T-cell receptor alpha chain variable region dominance in a peptide-specific response.	
#journal		#cross-references GB:M84653; NID:g199287; PID:g199288	
#title		sequence extracted from NCBI backbone (NCBI:115311, NCBI:P:115312)	
#note		NCBI:P:115312	
#accession		A46242	
#status		Preliminary	
#molecule_type		nucleic acid	
#residues		1-115	#label NAT
#cross-references		GB:M84653; NID:g199287; PID:g199288	
#note		sequence extracted from NCBI backbone (NCBI:115311, NCBI:P:115312)	

CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	T-cell receptor
SUMMARY	#length 115 #checksum 6093

Query Match 100.0%; Score 38; DB 2; Length 115;
Best Local Similarity 83.3%; Pred. No. 1.96e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 38 DDFLFI 43
|||
Qy 1 DDFLXI 6

RESULT ENTRY TITLE	2	H64031	#type complete
ORGANISM		hypothetical protein H11487 - Haemophilus influenzae (strain Rd KW20)	
DATE		18-Aug-1995	#sequence_revision 18-Aug-1995
ACCESSIONS		10-Oct-1997	#text_change
REFERENCE		H64031	
#authors		Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kierlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;	

WORLD

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 2 14:22:02 1998; Maspar time 3.20 Seconds
Tabular output not generated. 79,803 Million cell updates/sec

Description: 1 CYDSIPR 7
Perfect Score: 59
Sequence: 1 CYDSIPR 7

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Watch 0s
Listing first 45 summaries

Database: 1.pir1 2.pir2 3.pir3 4.pir4 5.nr13d

Statistics: Mean 21.467; Variance 26.929; scale 0.797

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	100.0	884	2	S53396	hypothetical protein
2	49	83.1	108	2	A48924	forkhead transcription factor
3	49	83.1	579	1	W2BE34	gene 34 protein - hum
4	49	83.1	675	2	S60612	protein-tyrosine kinase
5	47	79.7	1035	2	S78199	probable maturase pro
6	46	78.0	195	2	A48190	non-actin-binding ABP
7	46	78.0	360	2	D44468	coenzyme F420 hydroge
8	46	78.0	2567	2	A49551	filamin, Mueller cell
9	45	76.3	59	5	LDTX	venom basic protein
10	45	76.3	59	1	VTEPIA	venom basic protein
11	45	76.3	608	2	S72177	dextranase (EC 3.2.1.1)
12	45	76.3	789	1	QBY32	ox13 intron 2 protein
13	45	76.3	854	2	S17995	gene COX1 intron 1 pr
14	44	74.6	211	2	S18463	lysozyme (EC 3.2.1.17)
15	44	74.6	288	2	C56281	7alpha-cephen-methoxy
16	44	74.6	304	2	G64175	hypothetical protein
17	44	74.6	340	1	B55973	transcription factor
18	44	74.6	349	1	I51739	transcription factor
19	44	74.6	358	1	I51735	transcription factor
20	44	74.6	358	1	A55973	transcription factor
21	44	74.6	359	1	I51734	transcription factor
22	44	74.6	363	1	C55973	transcription factor
23	44	74.6	447	1	AJECRS	argininosuccinate syn

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24 44 74.6 455 2 G01923 KIR (cl-5) NK recepto 3.43e+01
25 44 74.6 877 2 C64809 yb5B protein - Escher 3.43e+01
26 44 74.6 4639 2 A54794 dynein heavy chain, c 3.43e+01
27 43 72.9 274 2 S50190 phosphotransferase sy 5.34e+01
28 43 72.9 287 2 G69141 hypothetical protein 5.34e+01
29 43 72.9 364 2 S28612 catechol O-methyltran 5.34e+01
30 43 72.9 365 2 S18568 lignin-bispecific O-m 5.34e+01
31 43 72.9 366 2 S40146 catechol O-methyltran 5.34e+01
32 43 72.9 435 2 I39171 cyclin A/CDK2-associat 5.34e+01
33 43 72.9 490 2 S76169 hypothetical protein 5.34e+01
34 43 72.9 641 2 I50642 gammaFDP-B - chicken 5.34e+01
35 43 72.9 665 2 I50641 gammaFDP-A - chicken 5.34e+01
36 43 72.9 676 2 I50643 gammaFDP-C - chicken 5.34e+01
37 43 72.9 2368 2 S46005 ESK1 protein - yeast 5.34e+01
38 43 72.9 2616 2 A57096 nudel protein precurs 5.34e+01
39 43 72.9 3791 1 YGPLV8 alpha-aminoadipyl-cys 5.34e+01
40 42 71.2 199 2 S23379 desiccation stress-in 8.26e+01
41 42 71.2 322 2 S23054 SPl protein - fruit f 8.26e+01
42 42 71.2 322 2 S23053 SPl protein - fruit f 8.26e+01
43 42 71.2 364 2 S36403 catechol O-methyltran 8.26e+01
44 42 71.2 516 2 S56604 hypothetical 58.0K pr 8.26e+01
45 42 71.2 638 1 KQRTPL plasma kallikrein (EC 8.26e+01

ALIGNMENTS

RESULT 1
ENTRY #S53396 #type complete
TITLE hypothetical protein YLR318w - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein L8543.12
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998

ACCESSIONS S53396
REFERENCE S53396
#authors Du, Z.
#submissions submitted to the EMBL Data Library, February 1995
#description The sequence of S. cerevisiae cosmid 8543.
#accession S53396
#molecule_type DNA

#residues 1-884 #label DUZ
#cross-references EMBL:U02618; NID:g2258165; PID:g662136; MIPS:YLR318w
#experimental_source strain S288C (AB972)
GENETICS
#gene SGD:EST2
#map_position 12R
#cross-references SGD:S0004310; MIPS:YLR318w
SUMMARY #length 884 #molecular-weight 102662 #checksum 7604

Query Match 100.0%; Score 59; DB 2; Length 884;
Best Local Similarity 100.0%; Pred. No. 2.09e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 534 CYDSIPR 540
Qy 1 CYDSIPR 7
|||||||

RESULT 2
ENTRY A48924 #type fragment
TITLE forkhead transcription activator homolog (clone FKX 5-3) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997

ACCESSIONS A48924
REFERENCE A48924
#authors Hromas, R.; Moore, J.; Johnston, T.; Socha, C.; Klemenz, M.
#journal Blood (1993) 81:2854-2859
#title Drosophila forkhead homologues are expressed in a lineage-restricted manner in human hematopoietic cells.
#cross-references MUID:93271467

FILE COPY

M I S R E H

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 2 14:09:49 1998; MasPar time 3.06 Seconds
Tabular output not generated. 71.676 Million cell updates/sec

T: 4 205-08-851-843-71
Description: 4 155 from US08851843.pep
Perfect Score: 45
Sequence: 1 FFYATE 6

Scoring table: PAM 150
Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 4 4:pir56
4 4:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.976; Variance 35.790; scale 0.586

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	45	100.0	87	2 S39696	hypothetical protein	9.72e+01
2	45	100.0	298	2 S53483	probable membrane pro	9.72e+01
3	45	100.0	343	2 S34811	matig factor MAT1-2	9.72e+01
4	45	100.0	343	2 S39588	3,4-dihydroxyphenylac	9.72e+01
5	45	100.0	709	2 E64213	DNA topoisomerase (EC	9.72e+01
6	45	100.0	884	2 S53396	hypothetical protein	9.72e+02
7	44	97.8	379	2 S27502	adenine deaminase hom	1.37e+02
8	44	97.8	580	2 H69793	1-phosphatidylglycosito	1.37e+02
9	44	97.8	1173	2 A33430	1-phosphatidylglycosito	1.37e+02
10	44	97.8	1216	2 A28821	1-phosphatidylglycosito	1.37e+02
11	44	97.8	1216	2 A28822	1-phosphatidylglycosito	1.37e+02
12	44	97.8	1571	2 S50669	hypothetical protein	1.37e+02
13	44	97.8	1591	2 A54146	invasion-inducing pro	1.37e+02
14	44	97.8	2178	2 S29237	calcium channel prote	1.37e+02
15	44	97.8	2206	2 JG5280	voltage-dependent cal	1.37e+02
16	44	97.8	2222	2 A47447	calcium channel prote	1.37e+02
17	44	97.8	2251	2 B54972	voltage-dependent cal	1.37e+02
18	44	97.8	2259	2 S29236	calcium channel prote	1.37e+02
19	44	97.8	2270	2 A54972	voltage-dependent cal	1.37e+02
20	44	97.8	2272	2 S54972	voltage-dependent cal	1.37e+02
21	44	97.8	2280	2 S41080	calcium channel alpha	1.37e+02
22	44	97.8	2288	2 S41080	calcium channel alpha	1.37e+02
23	44	97.8	2326	2 B47447	calcium channel prote	1.37e+02

24	44	97.8	2336	2 A45386	omega-conotoxin-sensi	1.37e+02
25	44	97.8	2339	2 A42566	omega-conotoxin-sensi	1.37e+02
26	42	93.3	254	1 UESY27	vegetative storage pr	2.71e+02
27	42	93.3	343	2 S66173	matig factor MAT-2 h	2.71e+02
28	42	93.3	355	2 G02532	aryldialkylphosphatas	2.71e+02
29	42	93.3	355	2 A45451	aryldialkylphosphatas	2.71e+02
30	42	93.3	517	2 A44483	protein disulfide iso	2.71e+02
31	42	93.3	544	2 G69992	spore cortex protein	2.71e+02
32	42	93.3	632	1 VGVNSY	surface glycoprotein	2.71e+02
33	42	93.3	651	2 A39372	potassium channel pro	2.71e+02
34	42	93.3	658	2 S60170	protein kinase Pak1 -	2.71e+02
35	42	93.3	673	2 S53604	maturase-related prot	2.71e+02
36	42	93.3	678	2 B38489	maturase-related prot	2.71e+02
37	42	93.3	736	1 VPXRPC	outer layer protein v	2.71e+02
38	42	93.3	863	2 B64138	uridylyltransferase h	2.71e+02
39	42	93.3	1006	2 S20126	exoribonuclease RAT1	2.71e+02
40	42	93.3	1337	2 B64993	hypothetical protein	2.71e+02
41	42	93.3	1363	2 A55875	xanthine dehydrogenas	2.71e+02
42	42	93.3	1603	1 VJKW5	vitellogenin 5 precu	2.71e+02
43	41	91.1	475	1 UBFFG	tubulin gamma chain -	3.77e+02
44	41	91.1	645	1 ODPP1	cytochrome-c oxidase	3.77e+02
45	41	91.1	856	2 A64699	hypothetical protein	3.77e+02

ALIGNMENTS

RESULT 1
ENTRY S39696 #type complete
TITLE hypothetical protein ywcE - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jan-1998

ACCESSIONS S39696; H70052
REFERENCE S39655
#authors Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, M.; Lubochinsky, B.; Marcelino, L.; Moszer, I.; Presecan, E.; Santana, M.; Schneider, E.; Schweizer, J.; Vertes, A.; Rapoport, G.; Danchin, A.
#journal Mol. Microbiol. (1993) 10:371-384
#title Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees.
#status S39696
#molecule_type DNA
#residues 1-87 #label GLA
#cross-references EMBL:X73124; NID:g413923; PID:g413965
#note the nucleotide sequence was submitted to the EMBL Data Library, //

REFERENCE

A69580
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Gollightly, E.J.; Grandi, G.; Gulseppi, G.; Guy, B.J.; Haga, K.; Haisch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Kjaer-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Orawa, K.; Ogilvara, A.; Oudega, B.; Park, S.; Parro, V.; Pohl, T.M.; Portetalle, D.; Porvqlk, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;

Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

H7002

#journal

#title

#accession

#status

#molecule_type DNA

#residues 1-87 #label KUN

#experimental_source strain 168

GENETICS

#gene

KEYWORDS

Summary

#length 87 #molecular-weight 9959 #checksum 2359

Query Match 100.0%; Score 45; DB 2; Length 87;

Best Local Similarity 83.3%; Pred. No. 9.72e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 42 FFYATE 47

||| ||

QY 1 FFYXTE 6

RESULT 2

ENTRY

TITLE

#type complete

Problem membrane protein YAR031w - yeast (Saccharomycetes cerevisiae)

#formal_name Saccharomycetes cerevisiae

05-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Nov-1997

ACCESSIONS

REFERENCE

#authors

#submission

#description

Sequencing of chromosome I of *Saccharomycetes cerevisiae*: analysis of the 52kbp CDC15- FLO1-PHO11-YAR074 region.

#accession

#molecule_type DNA

#residues 1-298 #label BUS

#cross-references EMBL:L28920; NID:g1616966; PID:g456136; MIPS:YAR031w

GENETICS

map_position 1R

KEYWORDS

transmembrane protein.

FEATURE

114-130

#domain transmembrane #status predicted #label TM1\

141-157

#domain transmembrane #status predicted #label TM2

Summary

#length 298 #molecular-weight 35073 #checksum 6036

Query Match 100.0%; Score 45; DB 2; Length 298;

Best Local Similarity 83.3%; Pred. No. 9.72e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 129 FFYATE 134

||| ||

QY 1 FFYXTE 6

RESULT 3

ENTRY

TITLE

#type complete

mating factor MAT1-2 - fungus (Cochliobolus heterostrophus)

ORGANISM

DATE

#formal_name Cochliobolus heterostrophus, Bipolaris maydis

31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change

08-Sep-1997

ACCESSIONS

REFERENCE

#authors

#journal

#title

#accession

#status preliminary

#molecule_type DNA

#residues 1-343 #label TUR

#cross-references EMBL:X68398; NID:g2585; PID:g2586

GENETICS

#gene

MAT1-2

#introns

CLASSIFICATION

KEYWORDS

FEATURE

129-203

Summary

#domain HMG box homology #label HMG1

#length 343 #molecular-weight 38319 #checksum 1452

Query Match 100.0%; Score 45; DB 2; Length 343;

Best Local Similarity 83.3%; Pred. No. 9.72e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 289 FFYXTE 294

||| ||

QY 1 FFYXTE 6

RESULT 4

ENTRY

TITLE

#type complete

3,4-dihydroxyphenylacetate 2,3-dioxygenase - *Arthrobacter globiformis*

#formal_name *Arthrobacter globiformis*

19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references M01D:95173098

#accession

#status preliminary; translated from GB/EMBL/DBJ

#molecule_type DNA

#residues 1-343 #label RES

#cross-references EMBL:U19817; NID:g642055; PID:g642056

GENETICS

#gene mndd

Summary

#length 343 #molecular-weight 38861 #checksum 7961

Query Match 100.0%; Score 45; DB 2; Length 343;

Best Local Similarity 83.3%; Pred. No. 9.72e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 128 FFYXTE 133

||| ||

QY 1 FFYXTE 6

RESULT 5

ENTRY

TITLE

#type complete

DNA topoisomerase (EC 5.99.1.2) - *Mycoplasma genitalium* (SGC3)

ALTERNATE_NAMES

type 1 DNA topoisomerase

#formal_name *Mycoplasma genitalium*

ORGANISM

DATE

17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change

APPLICANT
COPY

FILE COPY

gene
CDS
BASE COUNT 978 a 456 c 541 g 775 t
ORIGIN
Query Match 20.3%; Score 535; DB 19; Length 2750;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 546; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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/clone.lib="p366, P. Hieter
/map="chromosome 12, 5.5 cm from CDC3; 10.7 cm from CDC25"
757..1977
/gene="BUD6"
/db_xref="SGD:L0002602"
757..1977
/gene="BUD6"
/codon_start=1
/db_xref="PID:g623610"
/translation="MNGTCTPVFLRIGDKTKKCVLPPTTKKPLRLFLIERFAYSFGANS
PDYIIMPOYGVFELELNLDIKEGFVIALKLENSNTIKFIDTVKIEISNQ
NDIIRHLEKMSFSAISKOTEPVLPQGLEANKHDLVQNKKDDDKTKIKIQIELGLI
KQVHINRSNINEIFNHLKVDNFSLFSKNSNRNMEKSTSHLSLSDLLSKVD
DLQVIEIMRKDVARRSQPKKLETVSKDLENAQADVLKQFIDTERKPHMKTWE
AELDKVEEQOFLVLELIDLEKALFETDLIKLACEQEKNSPKNPILP
IMRPTFNQVREQVAVQSLNPDHDSRVEAIDKAEMWEMERKLKATNEFDDELENF
VGNLKKSGGLK"

Db 13406 GTGGGTTGAAGATAAGTGTACATTAGAGAAGATGCTTTTTTCAGGGCTCTAGTTATC 13465
QY 1861 GTGGGTTGAAGATAAGTGTACATTAGAGAAGATGCTTTTTTCAGGGCTCTAGTTATC 1920
Db 13466 TCGTCCGATCGTTGATTTGGTGTATGACGATCTTCGGAGTTTATAGGAGTTAAAGC 13525
QY 1921 TCGTCCGATCGTTGATTTGGTGTATGACGATCTTCGGAGTTTATAGGAGTTAAAGC 1980
Db 13526 CAGTCTACGAGGACACATTAATTTTAAAGCTGCTGACGATTTCTTATATATCAAC 13585
QY 1981 CAGTCTACGAGGACACATTAATTTTAAAGCTGCTGACGATTTCTTATATATCAAC 2040
Db 13586 AGACCAACAGCAAGTATCAATATCAAAAGCTTGCCATGGCGGATTTCAAAAATATAA 13645
QY 2041 AGACCAACAGCAAGTATCAATATCAAAAGCTTGCCATGGCGGATTTCAAAAATATAA 2100
Db 13646 TCGGAAGCAATAGAGACAAAATTTAGCCGTAGCTCCCAATCAGATGATACGGT 13705
QY 2101 TCGGAAGCAATAGAGACAAAATTTAGCCGTAGCTCCCAATCAGATGATACGGT 2160
Db 13706 TATTCATTTTGTCAATGACATATTTGTTAAAGATTTGGAAGTTTGAACATTCAG 13765
QY 2161 TATTCATTTTGTCAATGACATATTTGTTAAAGATTTGGAAGTTTGAACATTCAG 2220
Db 13766 CACAATGAATATTTCCATATCCGTTTCAAAATCTAGTAAAGGATATTTGGAAGTTTAA 13825
QY 2221 CACAATGAATATTTCCATATCCGTTTCAAAATCTAGTAAAGGATATTTGGAAGTTTAA 2280
Db 13826 AGCGTGTTTAAGTATAGTATCTTATATAAACAATTTGACACAAAATTTAAATTCACAAA 13885
QY 2281 AGCGTGTTTAAGTATAGTATCTTATATAAACAATTTGACACAAAATTTAAATTCACAAA 2340
Db 13886 CACCGTCTCATGCAATGATCATGTTGTAAGAACATTTCCGATGTTTAAATTCACAAA 13945
QY 2341 CACCGTCTCATGCAATGATCATGTTGTAAGAACATTTCCGATGTTTAAATTCACAAA 2400
Db 13946 TTTAAGGATCTATCAATTAATTTACGCAAAATATGCAAAATTTCAATTTCTTACAACG 14005
QY 2401 TTTAAGGATCTATCAATTAATTTACGCAAAATATGCAAAATTTCAATTTCTTACAACG 2460
Db 14006 CATCATTTGAATGACAGTACGAGGTTGTCCTCAATTTACGAAATGATGATTTTAAATTCAGTA 14065
QY 2461 CATCATTTGAATGACAGTACGAGGTTGTCCTCAATTTACGAAATGATGATTTTAAATTCAGTA 2520
Db 14066 TGAGTACGATTCACATTTGAATGATTTTGAAGAGCTATCTTCAACACATCAAA 14125
QY 2521 TGAGTACGATTCACATTTGAATGATTTTGAAGAGCTATCTTCAACACATCAAA 2580
Db 14126 ATTTAAGATATATATCTTTTGAAGAGCTATCTTCAACACATTTCAACCTTGAAGC 14176
2581 ATTTAAGATATATATCTTTTGAAGAGCTATCTTCAACACATTTCAACCTTGAAGC 2631

RESULT 2 YSCPROT 2750 bp DNA PLN 26-JUL-1996
LOCUS Saccharomyces cerevisiae (clone H3.4) BUD6 gene, complete cds.
DEFINITION 91464752
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM Saccharomyces cerevisiae (clone library: p366, P. Hieter) DNA.
Eukaryotes; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
Saccharomycetes.
REFERENCE 1 (bases 1 to 2750)
AUTHORS Zahner, J.E. and Pringle, J.R.
TITLE Sequencing and characterization of BUD6
JOURNAL Unpublished (1995)
FEATURES
location/Qualifiers
1..2750
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"

FILE COP/APPLICANT COPY

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BASE COUNT	32 a	51 c	58 g	28 t	2 others
ORIGIN					
Query Match	6.2%; Score 24; DB 23; Length 171;				
Best Local Similarity	73.5%; Pred. NO. 9.22e-08;				
Matches	36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;				
Db	74	GCTCTTGGGCGCTGTGCAGCTGCTGCCGCTGGCCGGTGCCGAGGNCGG	122		
Qy	150	GCATTGAAGAGGTGTGCAGTCGGGACGTGTCCGAACGACAGAGGTCAAG	198		

RESULT	10						
LOCUS	R92606	394 bp	mRNA	EST			
DEFINITION	yq07g02.s1 Homo sapiens cDNA clone 196274 3'						25-AUG-1995

[illegible]

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: polyT not found
 Insert Length: 832 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 156.
 Location/Qualifiers
 1..171

FEATURES

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers

source

BASE COUNT	ORIGIN	MRNA	190274
91 a	85 c	73 g	143 t
<div> <div><1. >394</div> <div>2 others</div> </div>			

Query Match 6.2%; Score 24; DB 19; Length 394;
Best Local Similarity 74.0%; Pred. No. 9.22e-08;
Matches 37; Conservative 0; Mismatches 13; Indels 0; Caps 0;

Db 230 CTGATCTTTGTCTACTTCAATTAGCTGACGAGGCTTCTTTTCATGGCAC 279
||||| |||| | ||| | |||| | |||| | |||| | |||| |
Qy 19 CTGATGAGTGTTACGTCGCGAGCTGCTCAGGCTCTTTCTTTTATGTCAC 68

RESULT 11

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/lab_host="DH10B (ampicillin resistant)"

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